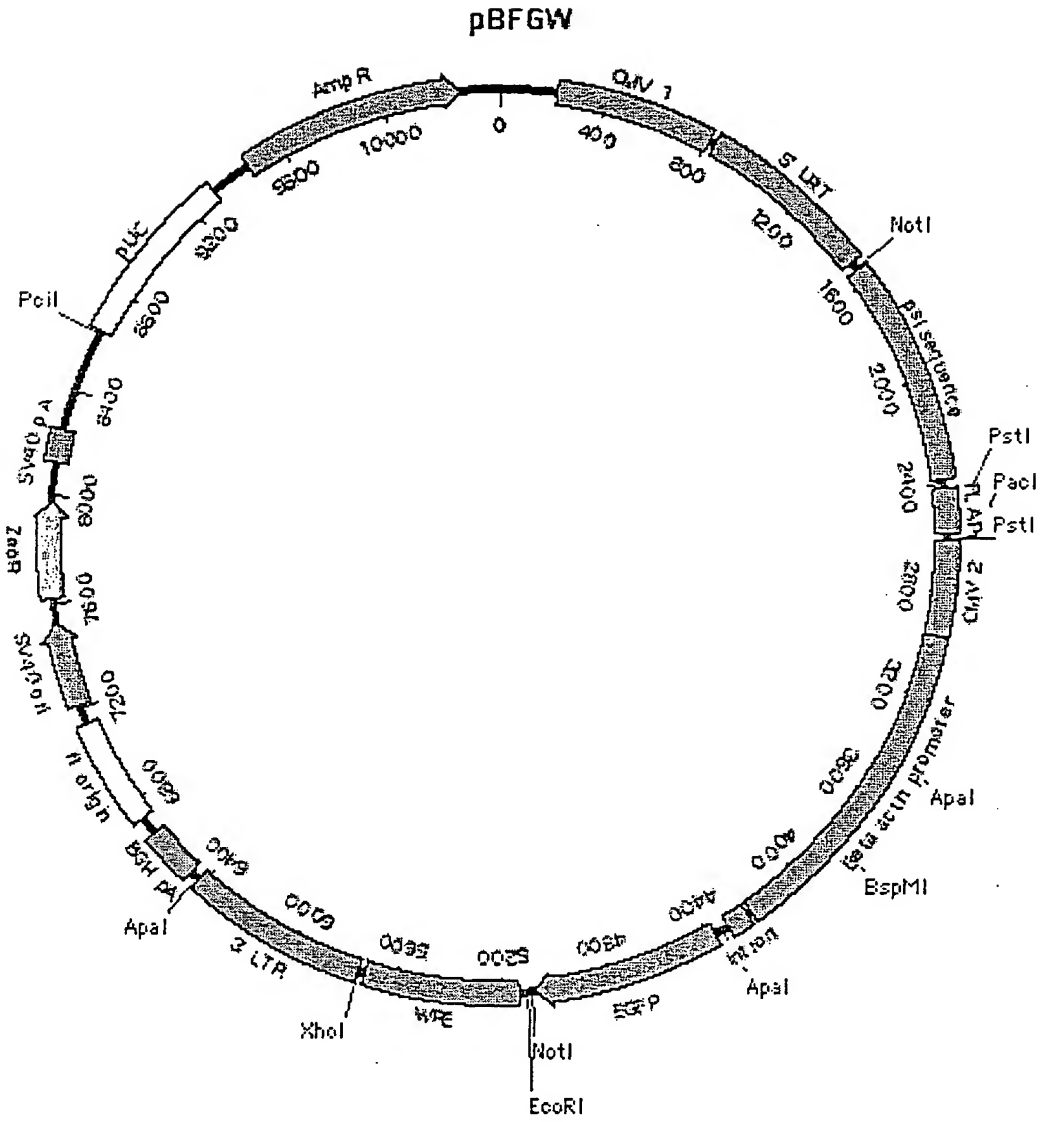


Figure 1

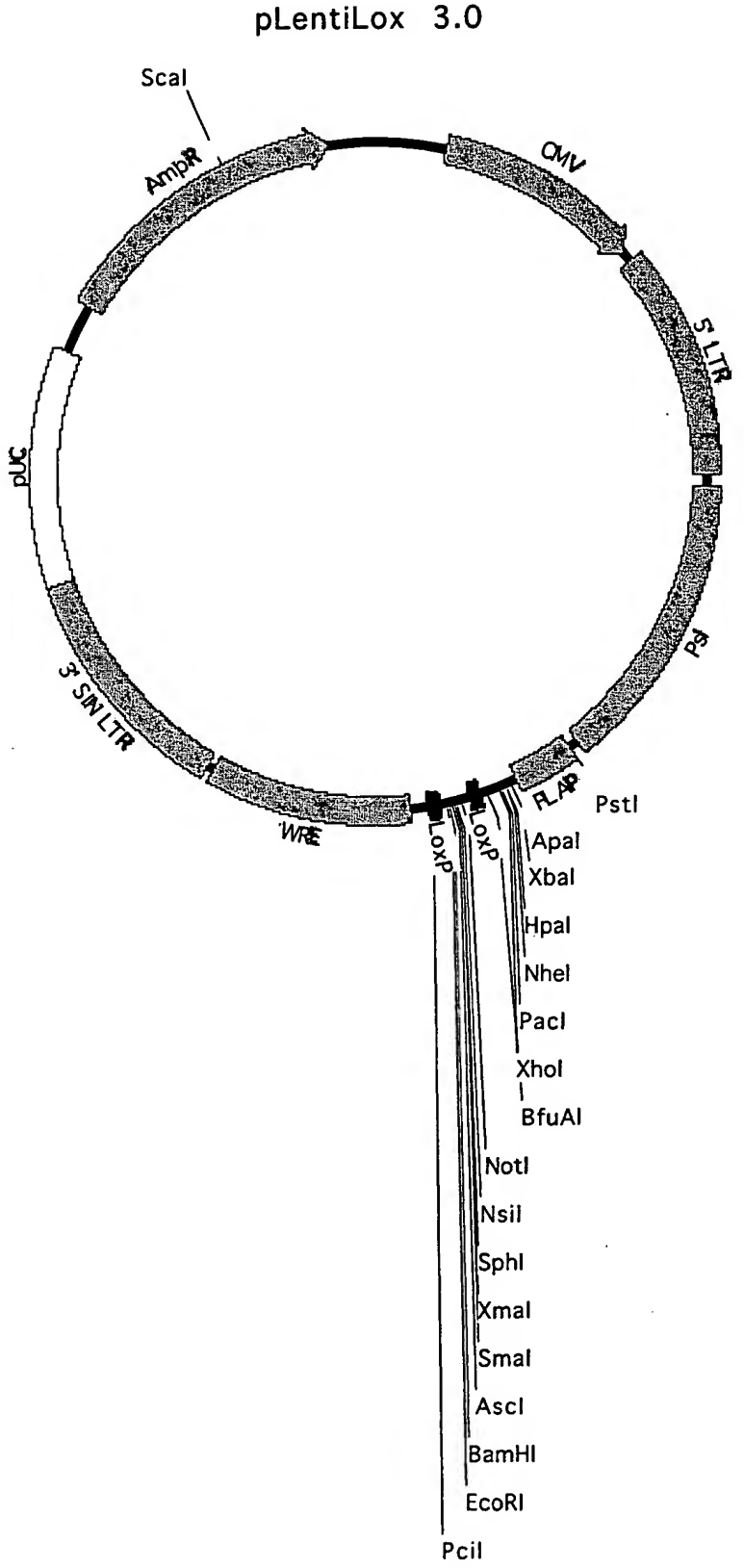

pLentiLox 3.0
ScaI
AmpR
CMV
5' LTR
Psi
RRE
PstI
ApaI
XbaI
HpaI
NheI
PacI
XhoI
BfuAI
NotI
NsiI
SphI
XmaI
SmaI
AscI
BamHI
EcoRI
PciI
LoxP
LoxP
3' SIN LTR
pUC

FIGURE 2

pLentiLox 3.1

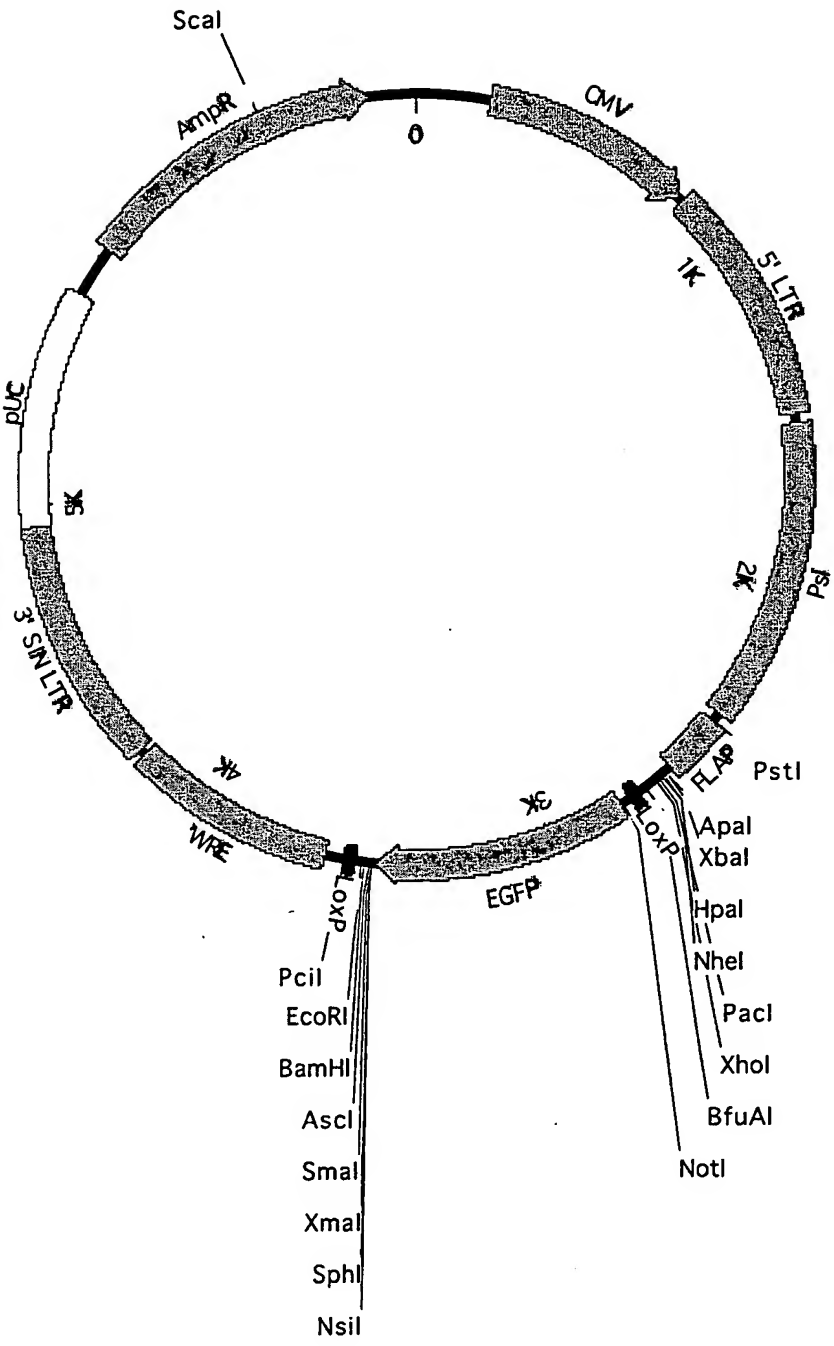


FIGURE 3

pLentiLox 3.2

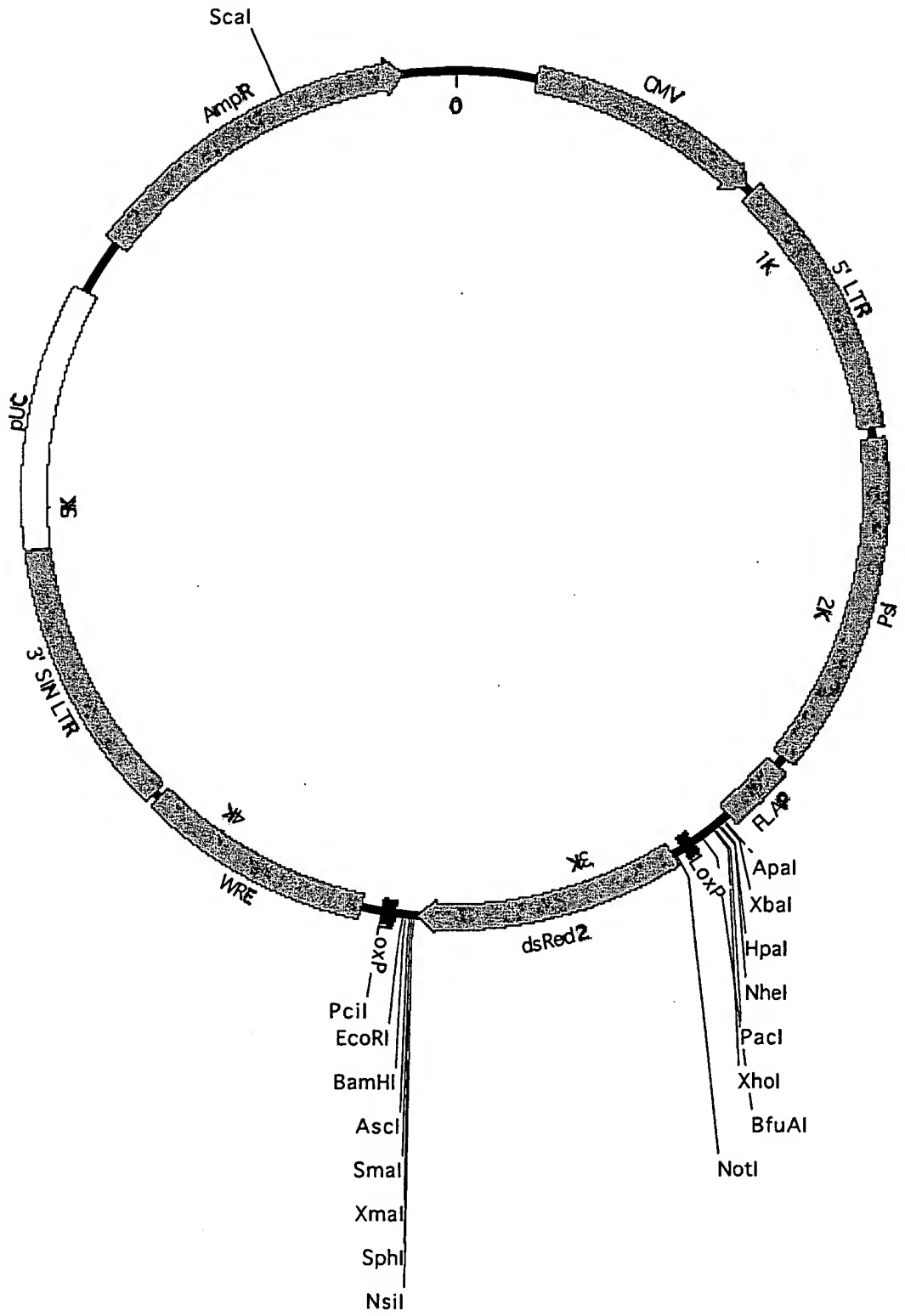


FIGURE 4

pLentiLox 3.3

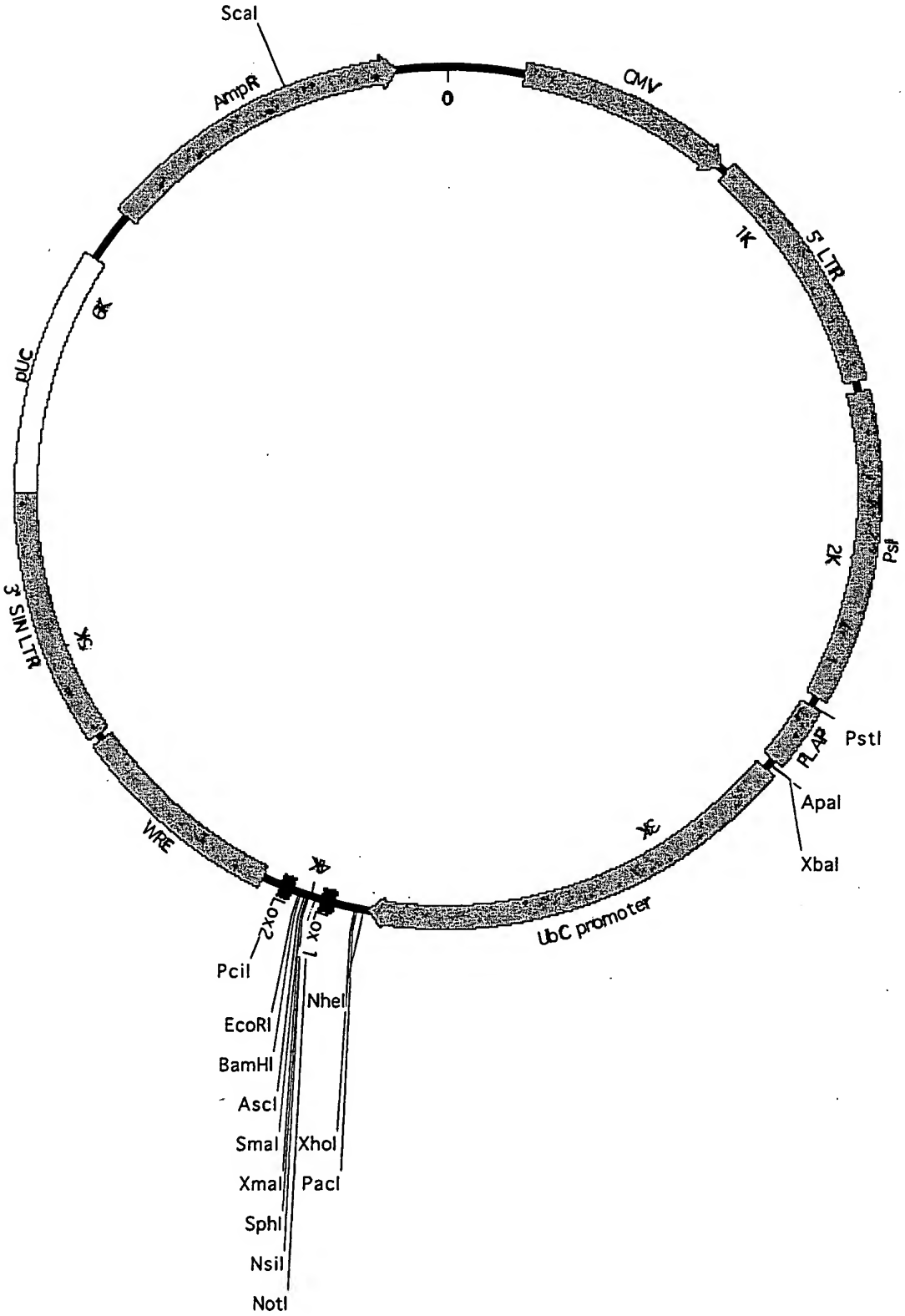


FIGURE 5

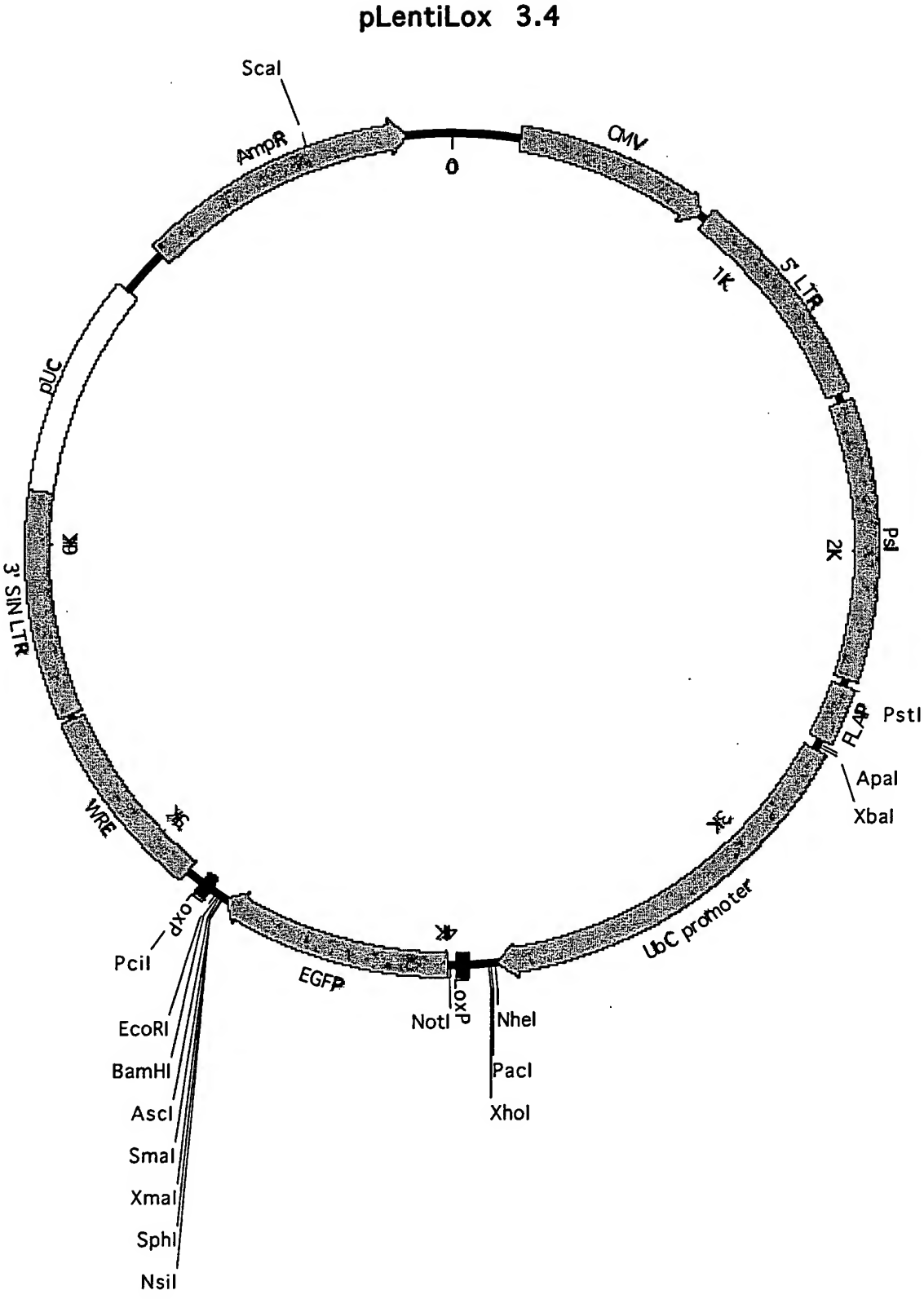

pLentiLox 3.4
ScaI
AmpR
0
CMV
5' LTR
1K
2K
PstI
R
U5
Apal
XbaI
UbC promoter
LoxP
NotI
NheI
PacI
XhoI
EGFP
cPPT
WRE
3' SIN LTR
pUC
PciI
EcoRI
BamHI
AscI
SmaI
XmaI
SphI
NsiI

FIGURE 6

pLentiLox 3.5

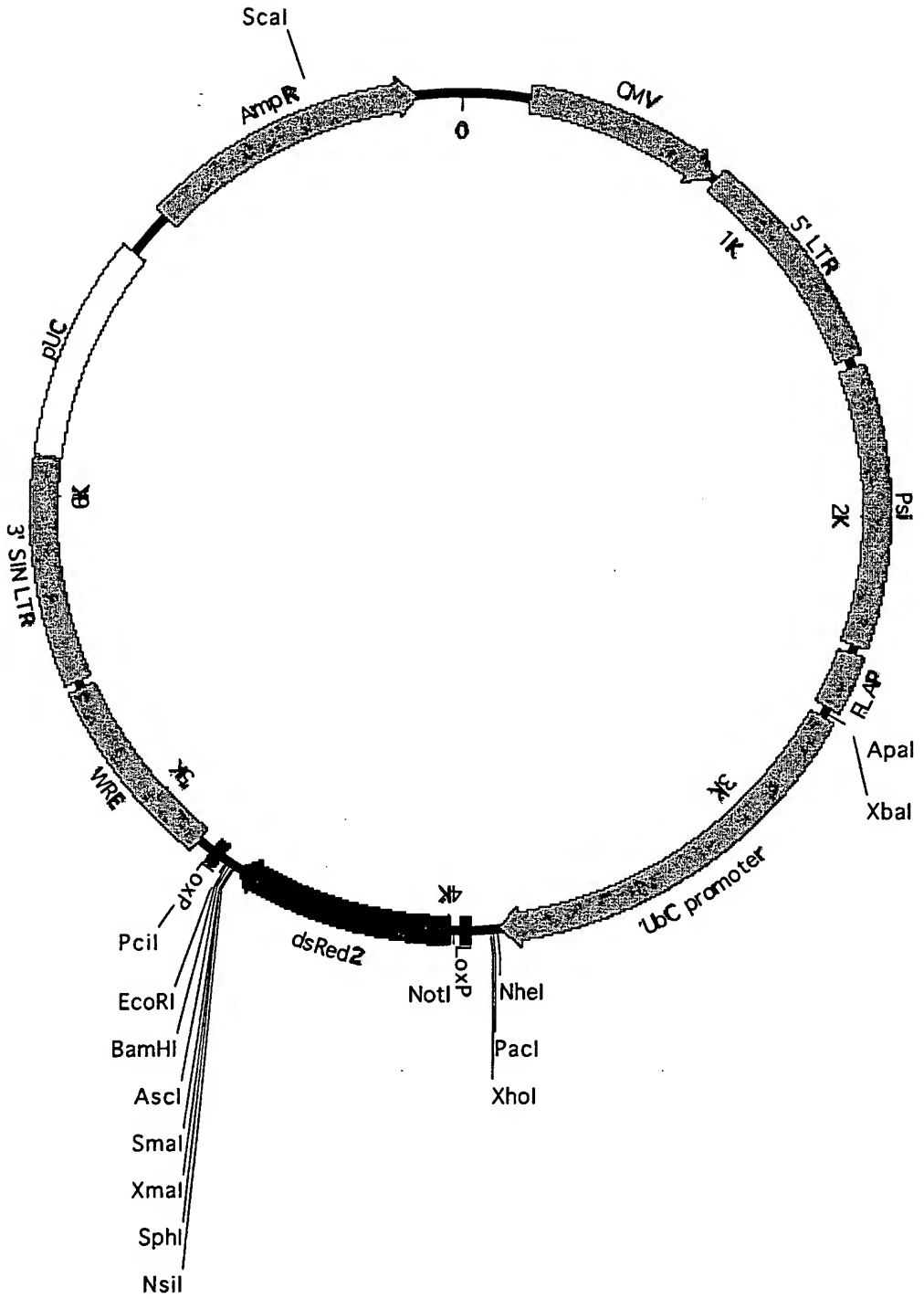


FIGURE 7

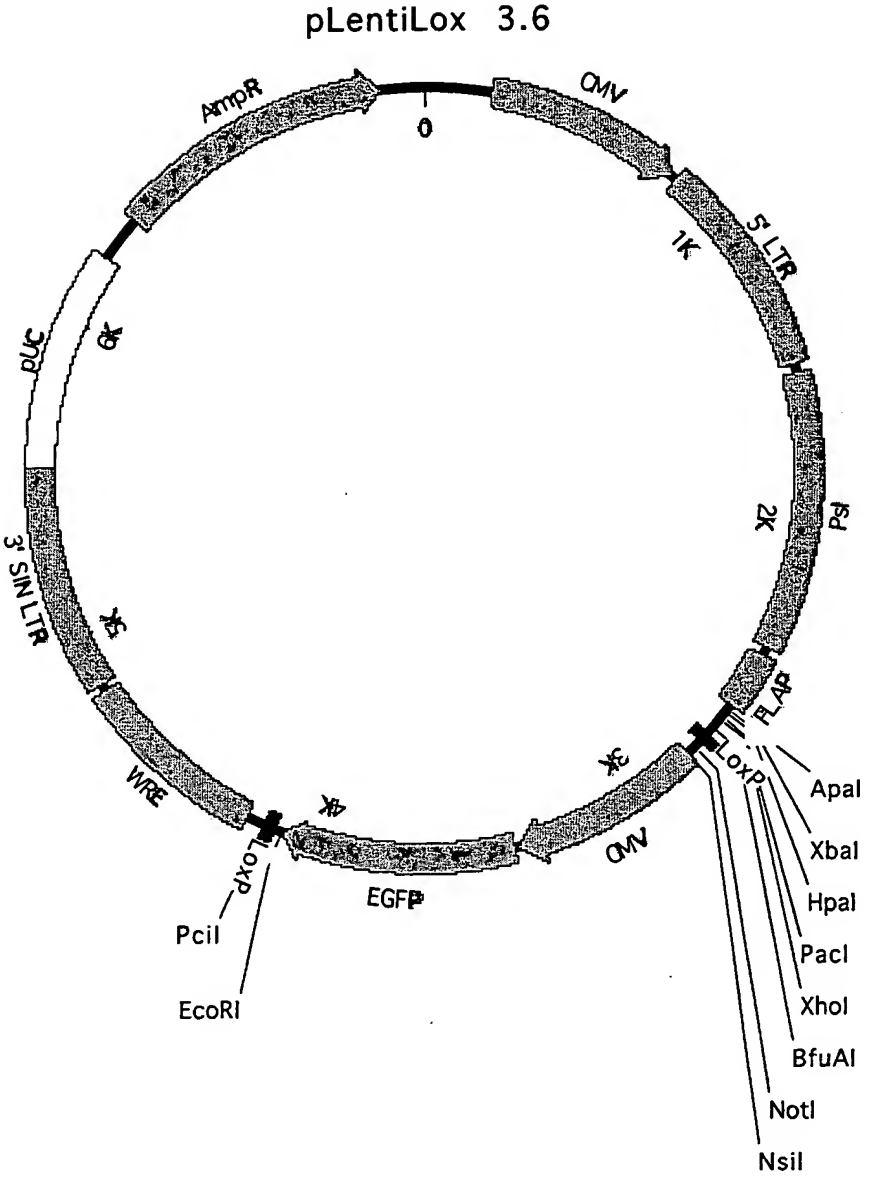

pLentiLox 3.6
AmpR
0
CMV
5' LTR
1K
2K
Psi
RLAP
LoxP
3K
CMV
EGFP
AK
LoxP
WRE
3' SIN LTR
PUC
ORI
ApaI
XbaI
HpaI
PacI
XhoI
BfuAI
NotI
NsiI
PciI
EcoRI

FIGURE 8

pLentiLox 3.7

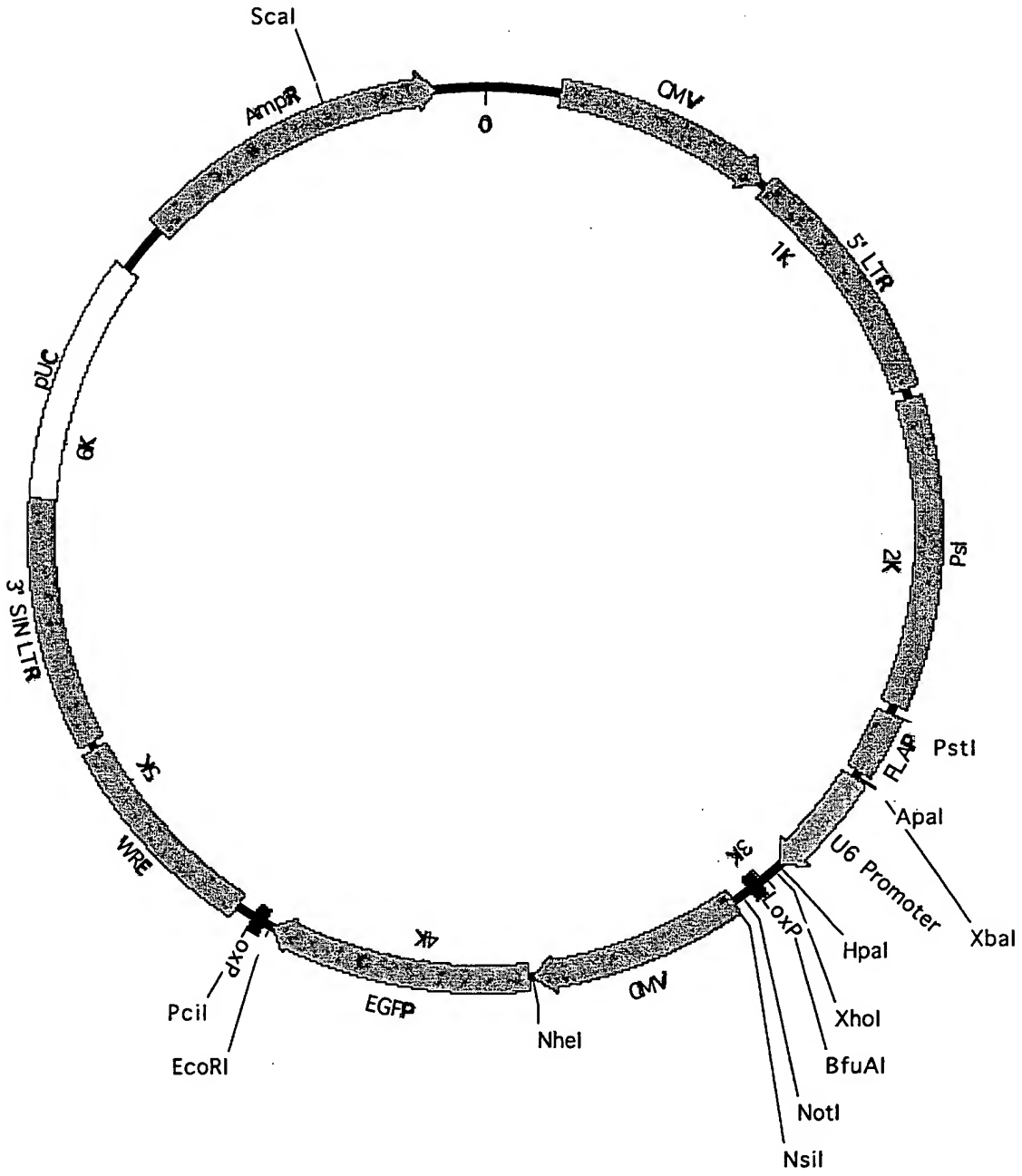


FIGURE 9

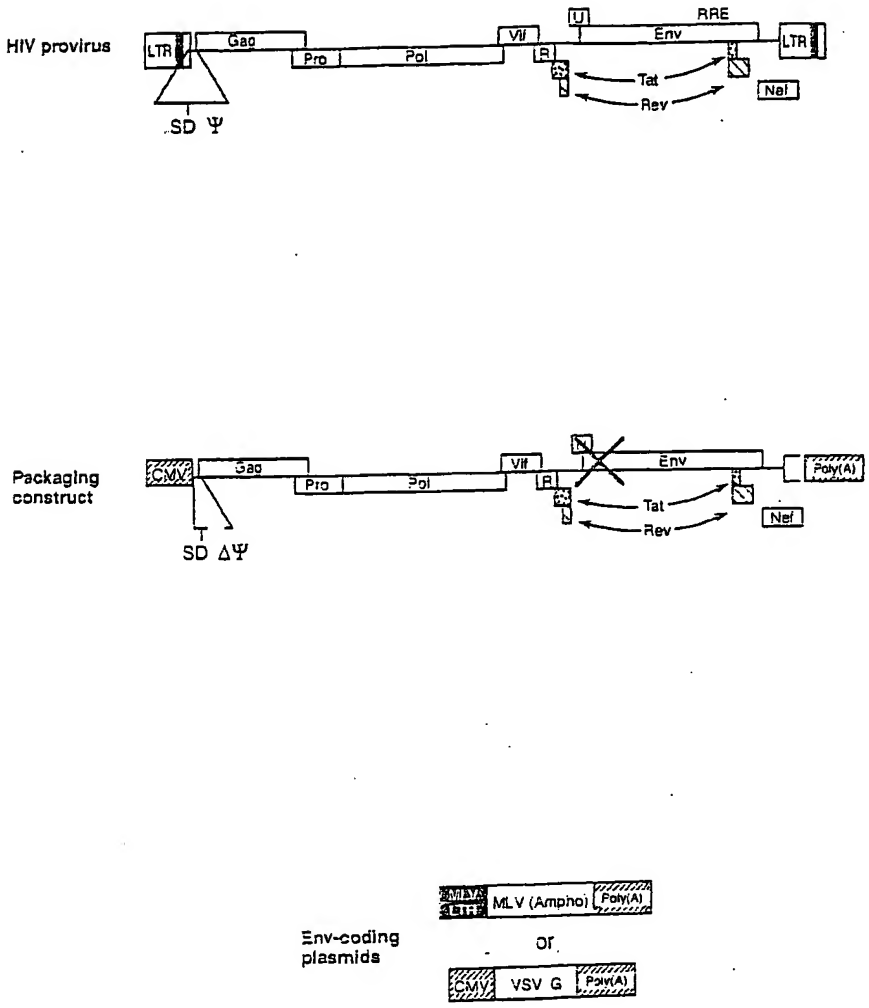
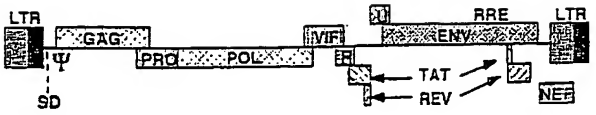
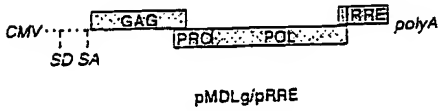

HIV provirus
LTR
Gag
Pro
Pol
Vif
U
RRE
Env
LTR
R
Tat
Rev
Nef
SD Ψ
Packaging construct
CMV
Gag
Pro
Pol
Vif
Env
Poly(A)
Tat
Rev
Nef
SD ΔΨ
Env-coding plasmids
MLV (Ampho)
Poly(A)
or
CMV
VSV G
Poly(A)

Figure 10 A

HIV Provirus

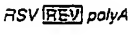


Packaging Construct



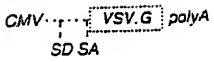
pMDLg/pRRE

Rev-coding Plasmid



RSV-Rev

Env-coding Plasmid



pMD.G

Figure 10B

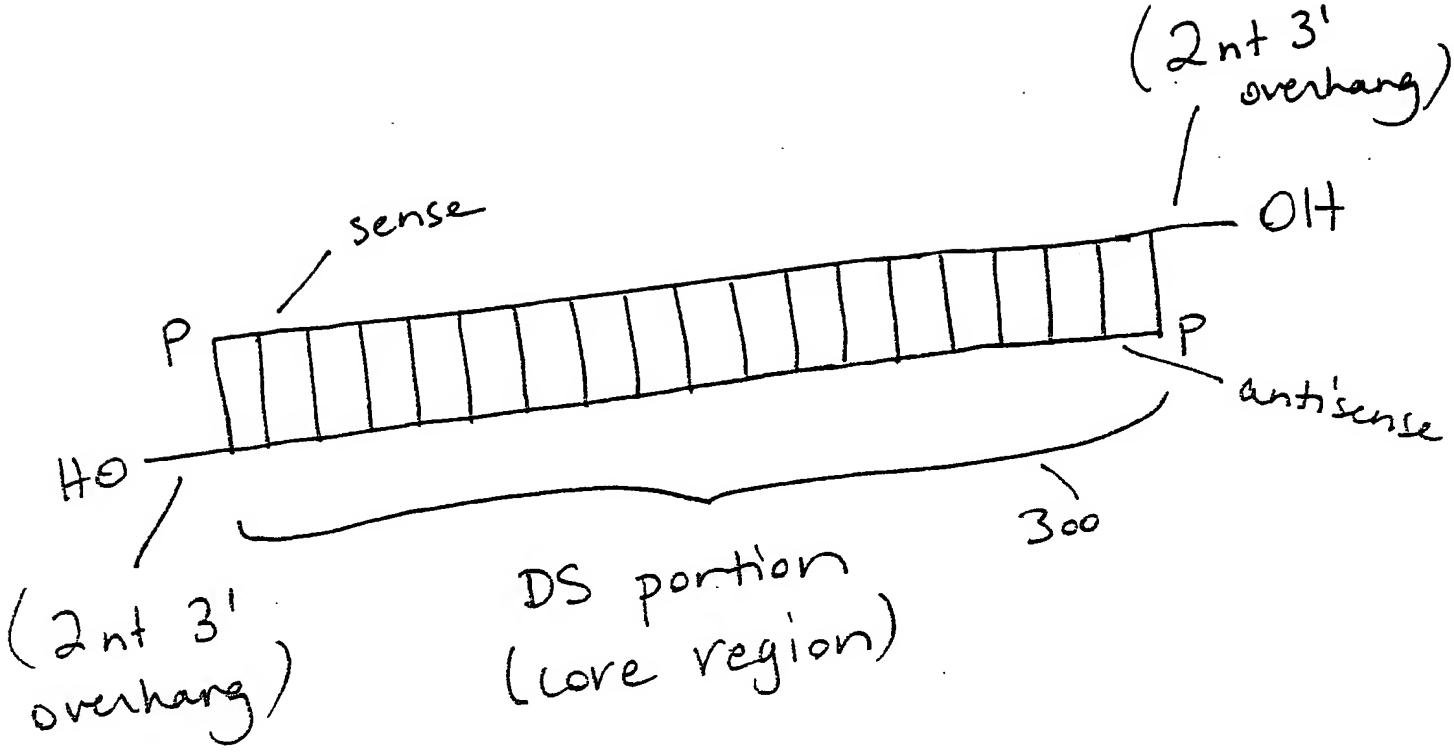

(2nt 3' overhang)
OH
sense
P
P
antisense
HO
300
(2nt 3' overhang)
DS portion
(core region)

Figure 11

RNAi in Drosophila

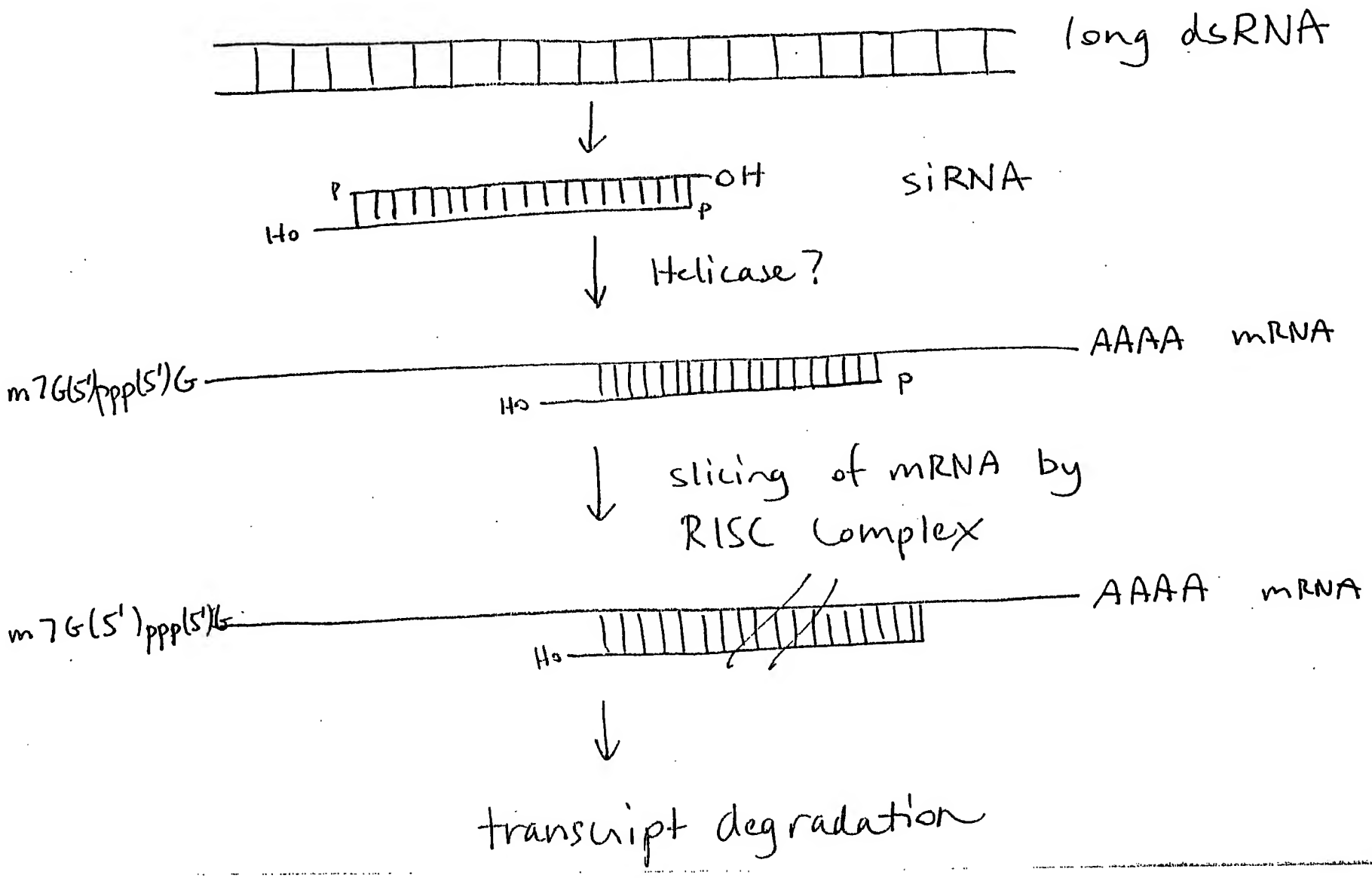


Figure 12

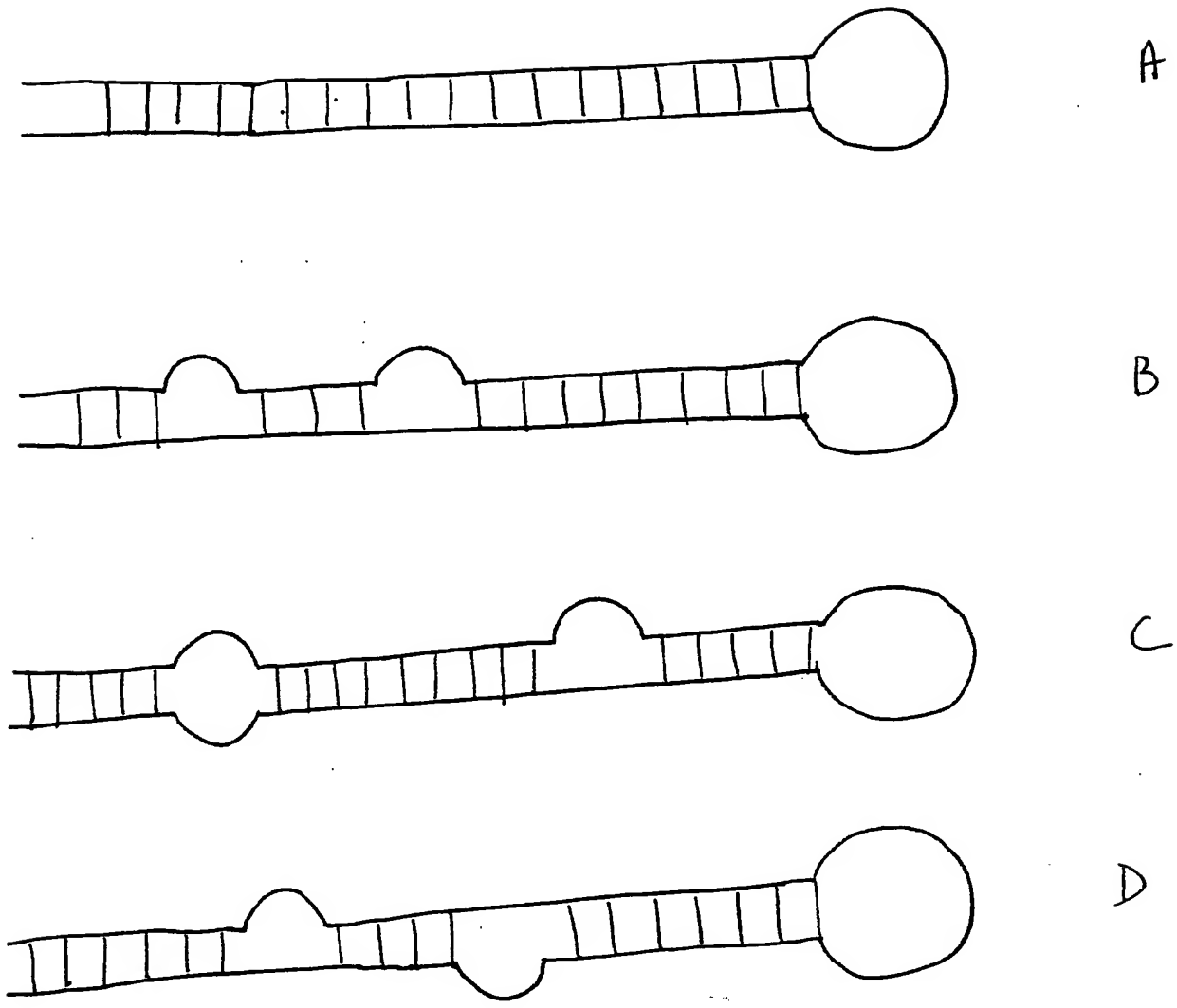


FIGURE 13

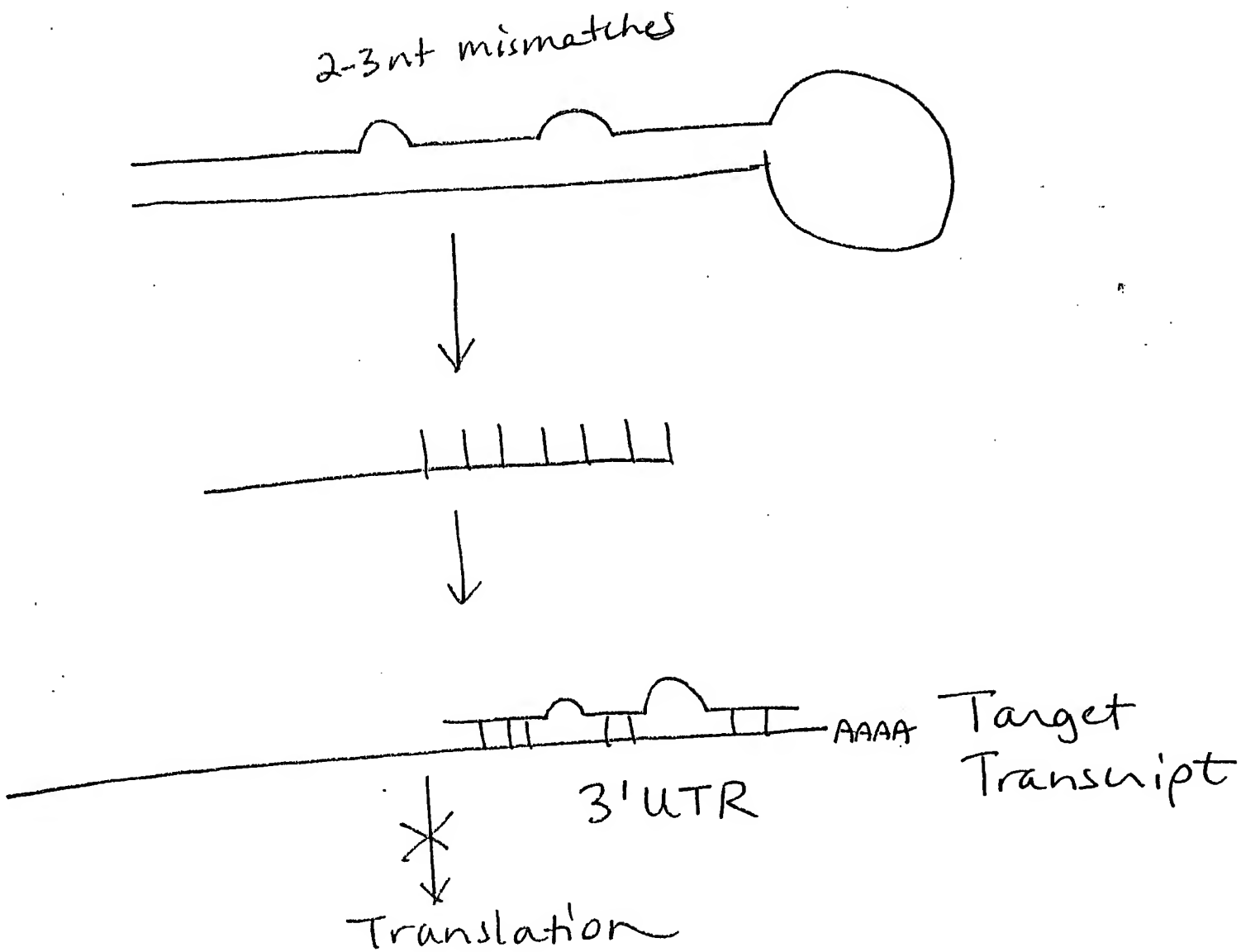


Figure 14

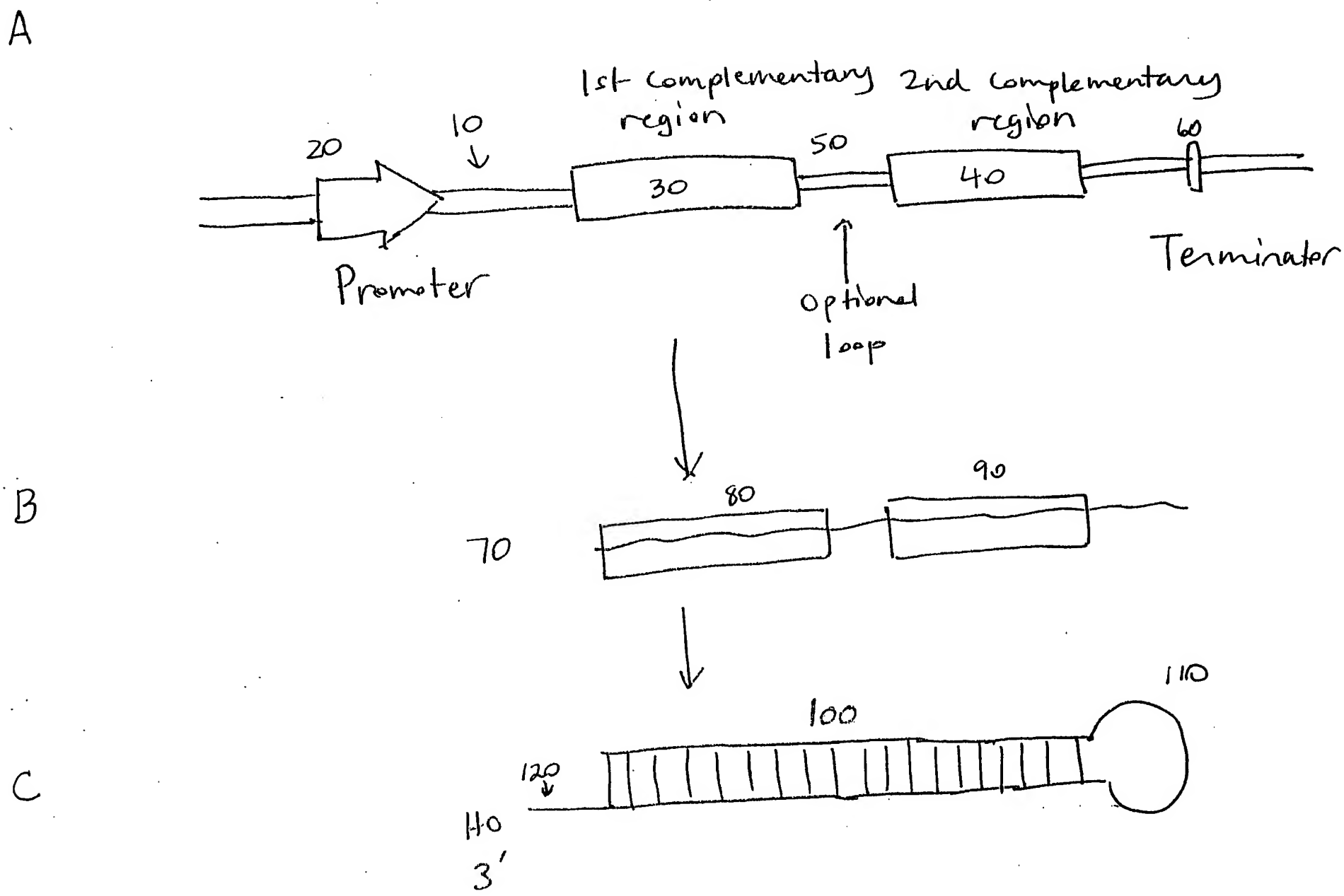

A
1st complementary region
2nd complementary region
10
20
30
40
50
60
Promoter
optional loop
Terminator
B
70
80
90
C
100
110
120
130
3'

Figure 15

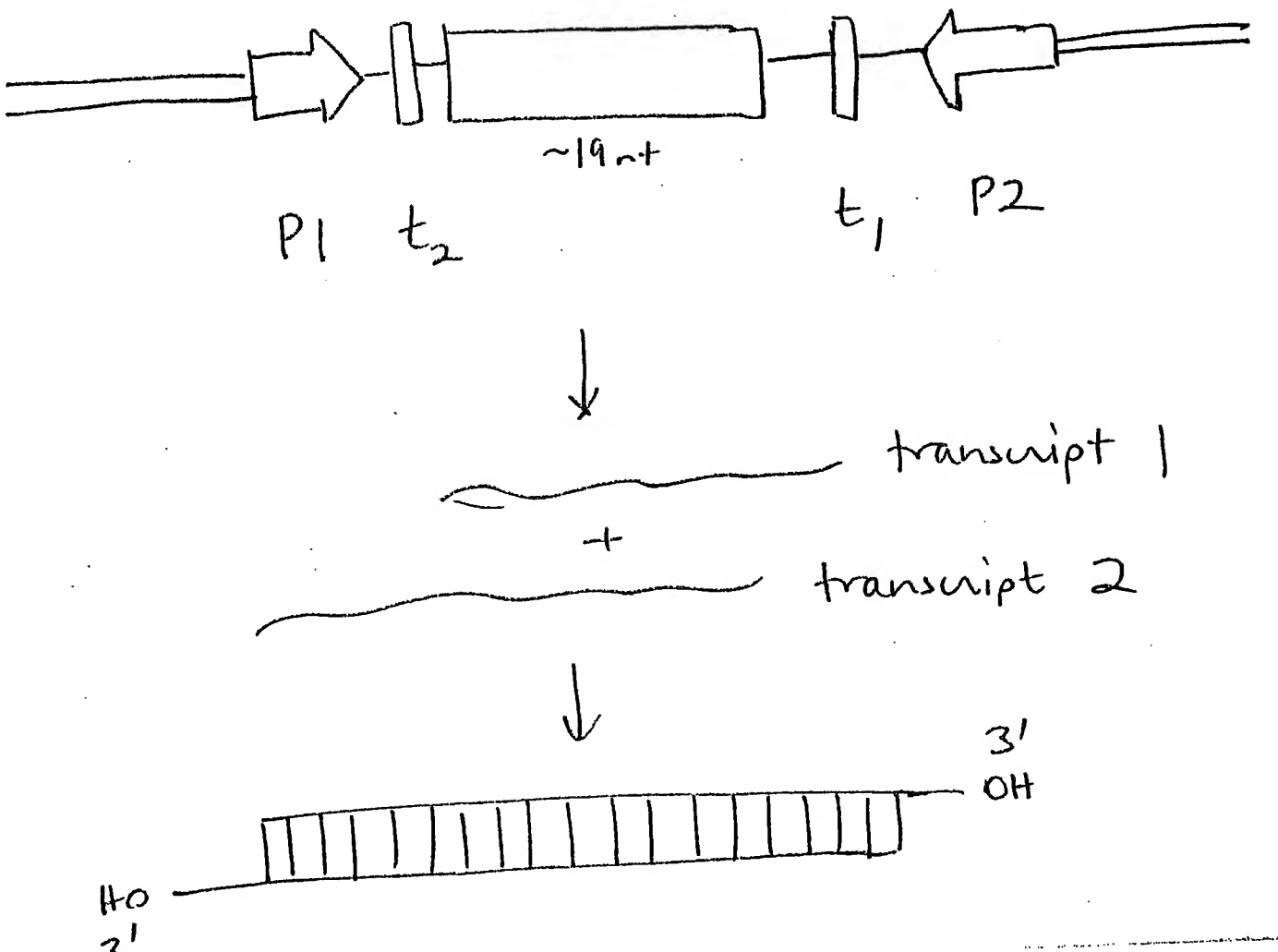
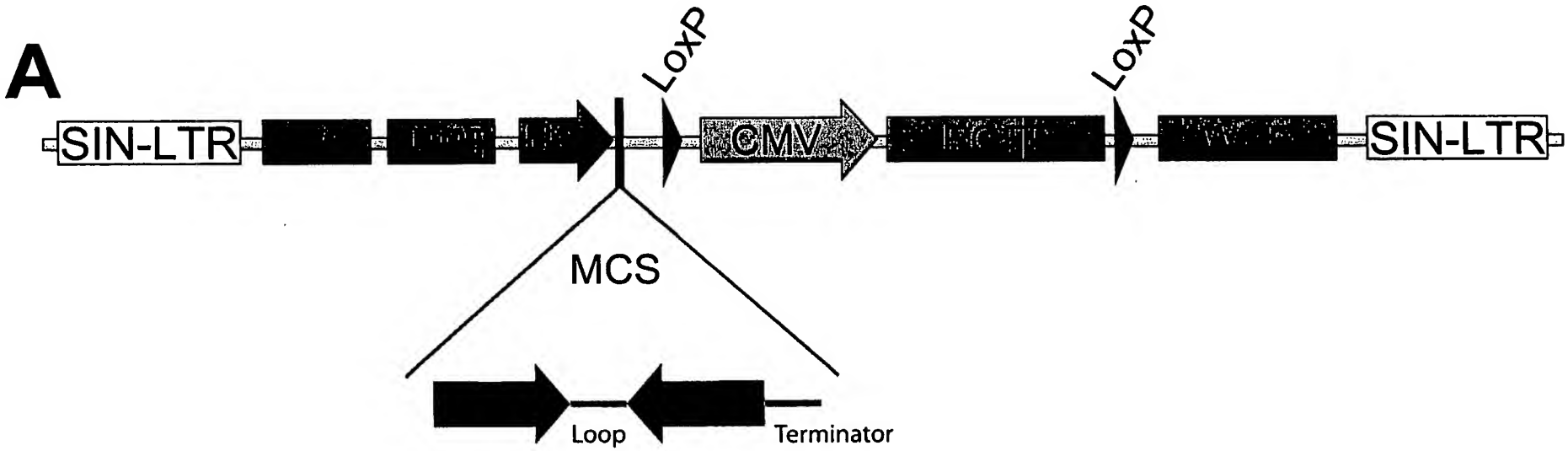


Figure 16

Figure 17



B CD8 Stem Loop Sequence

+1 Loop Terminator

TGCTACAACTACTACATGACTTCAAGAGAGTCATGTAGTAGTTGTAGCTTTTTTTG

ACGATGTTGATGATGTACTGAAGTTCTCTCAGTACATCATCAACATCGAAAAAACATTG

C Predicted CD8 Stem Loop

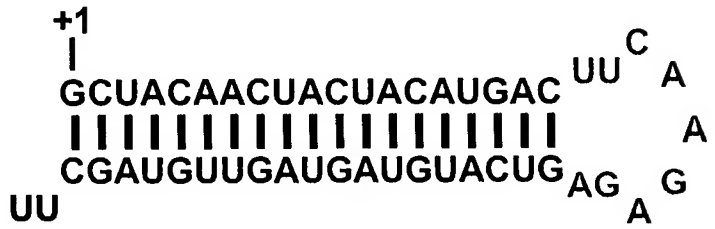


Figure 18

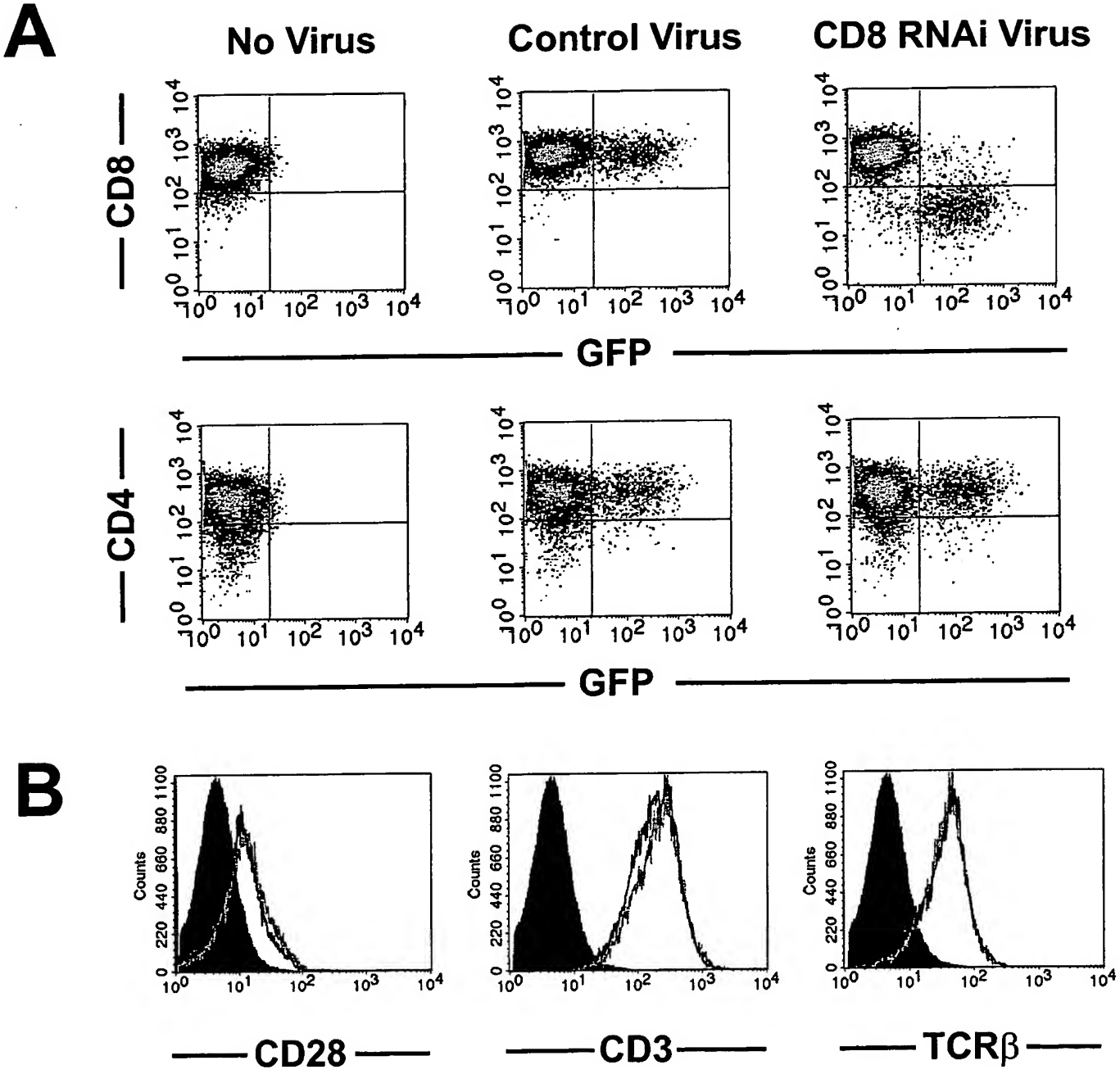
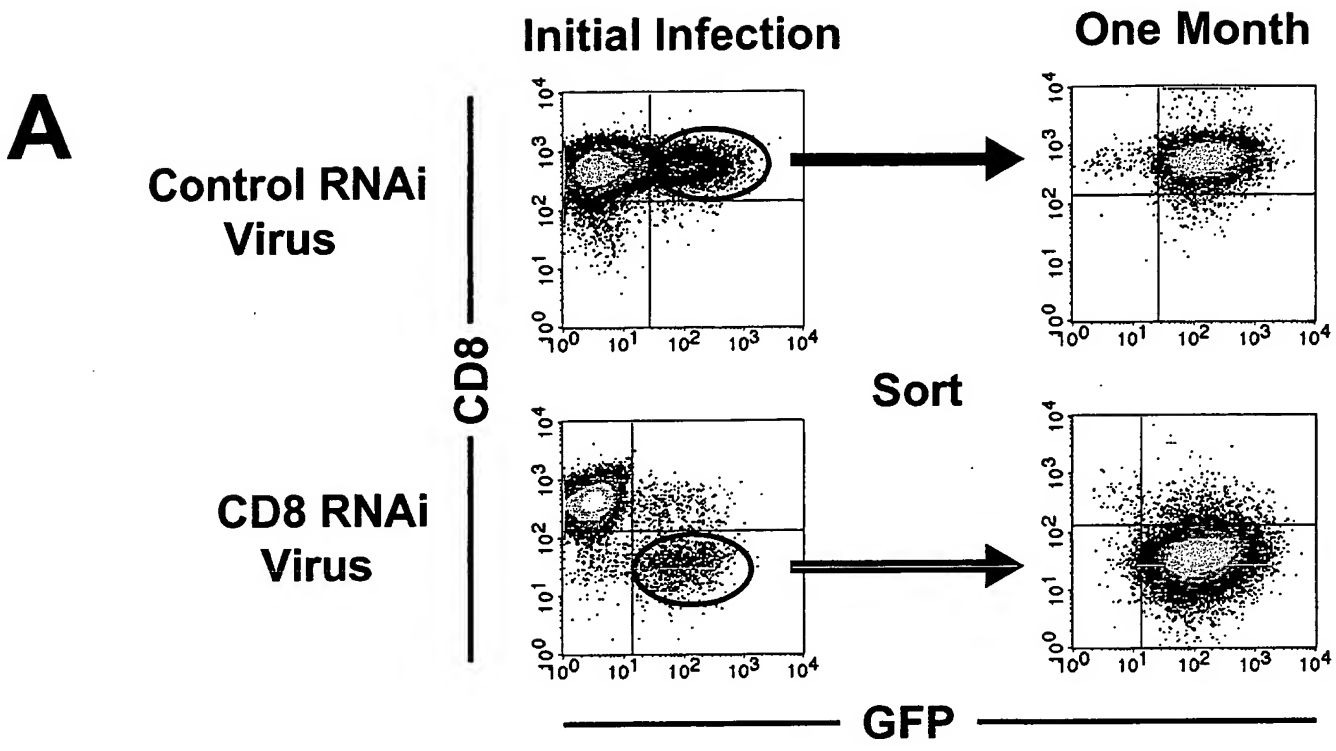
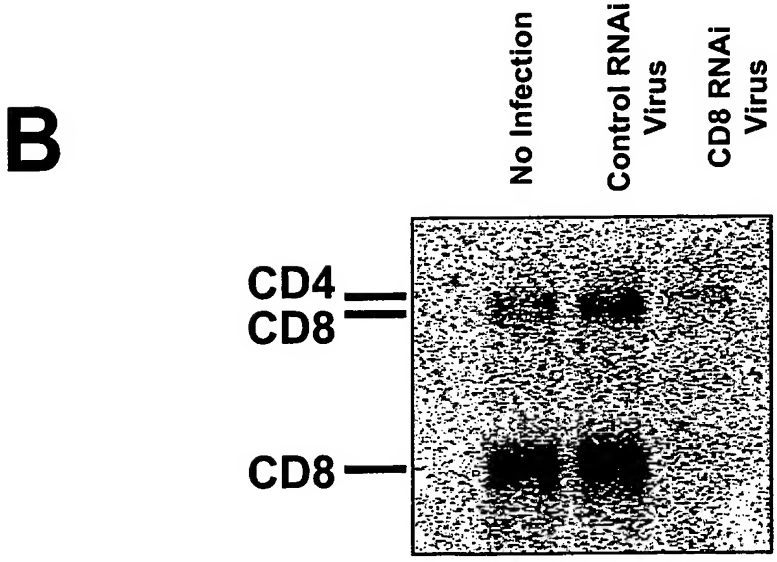

A
No Virus
Control Virus
CD8 RNAi Virus
CD8
GFP
CD4
GFP
B
Counts
CD28
CD3
TCRβ

Figure 19


A
Initial Infection
One Month
Control RNAi Virus
CD8 RNAi Virus
CD8
Sort
GFP


B
No Infection
Control RNAi Virus
CD8 RNAi Virus
CD4
CD8
CD8

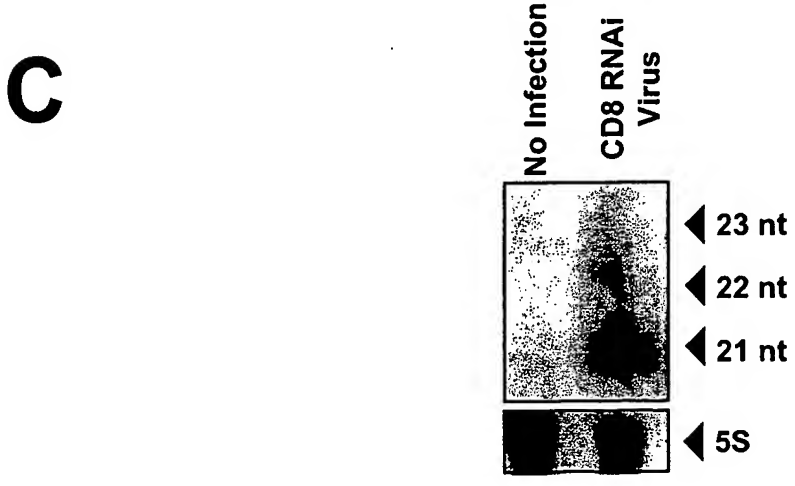
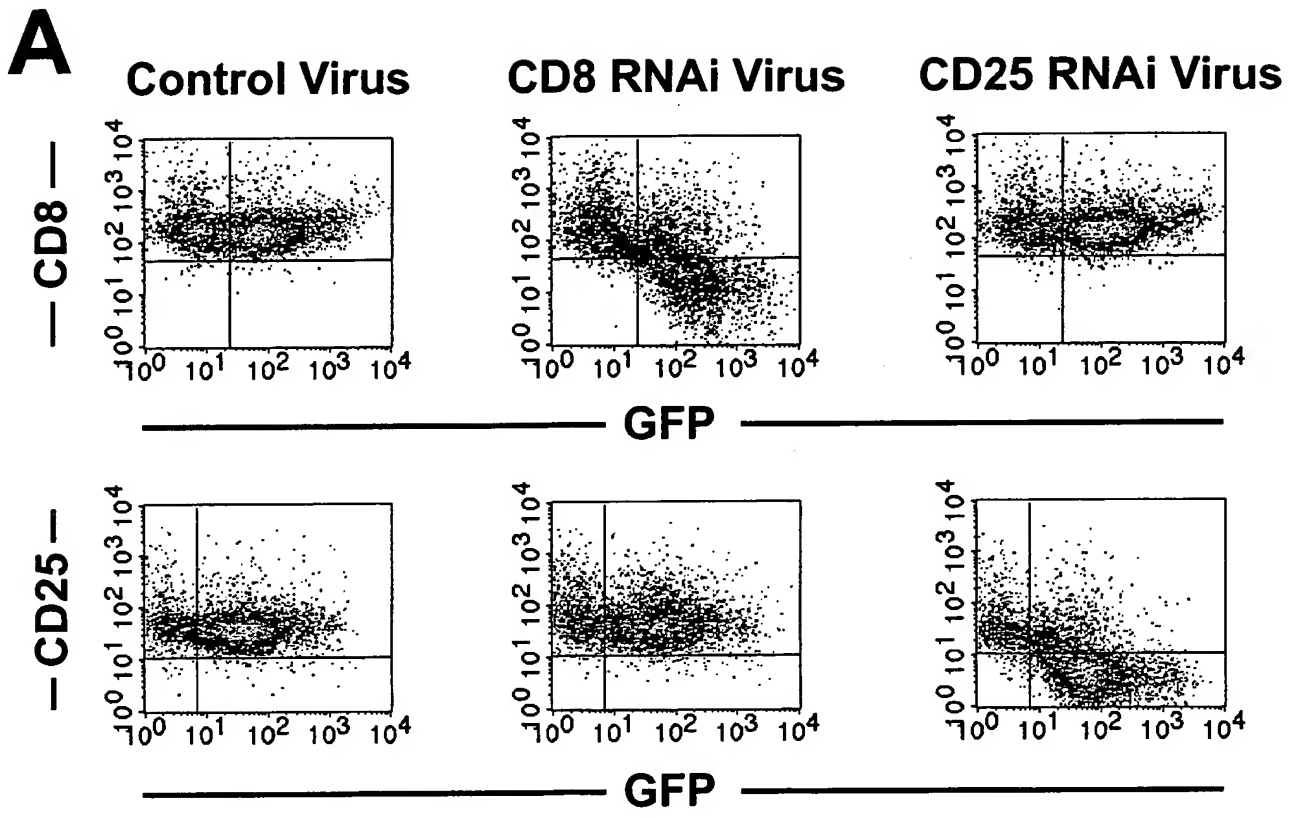

C
No Infection
CD8 RNAi Virus
23 nt
22 nt
21 nt
5S

Figure 20


A
Control Virus
CD8 RNAi Virus
CD25 RNAi Virus
CD8
CD25
GFP
GFP

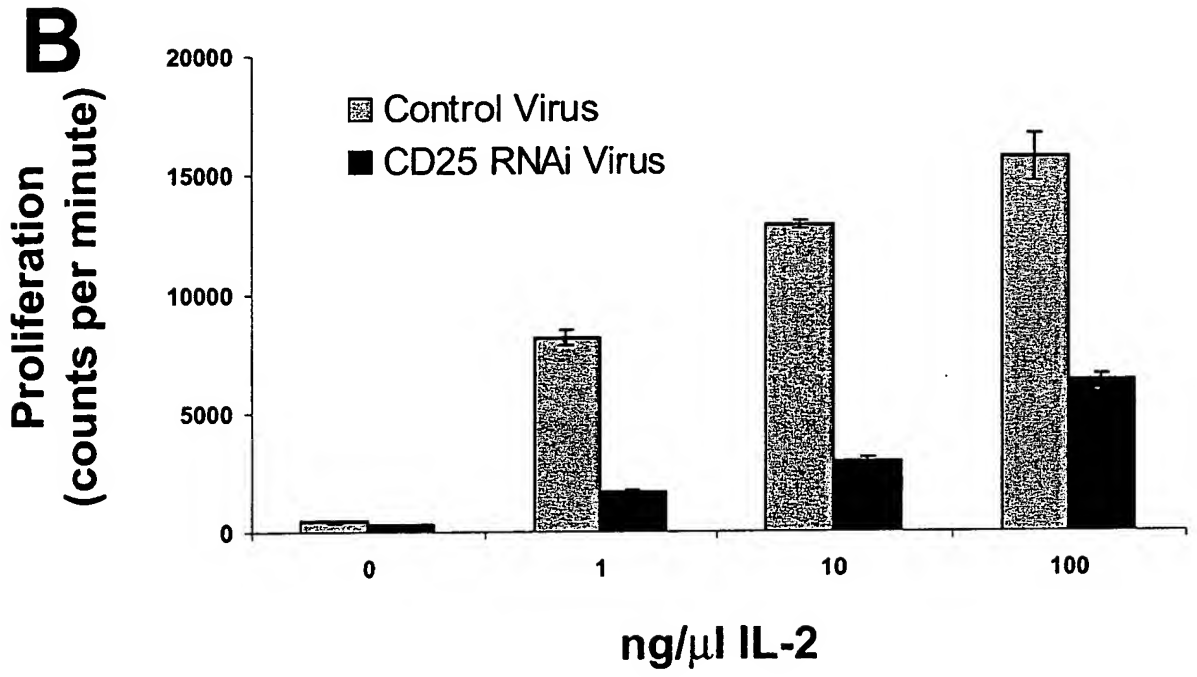
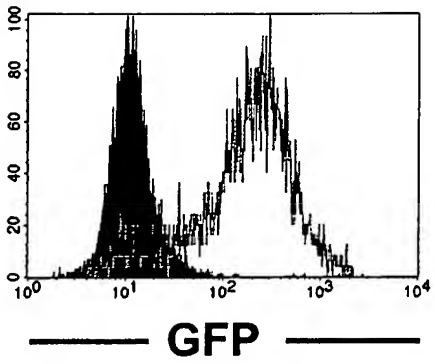
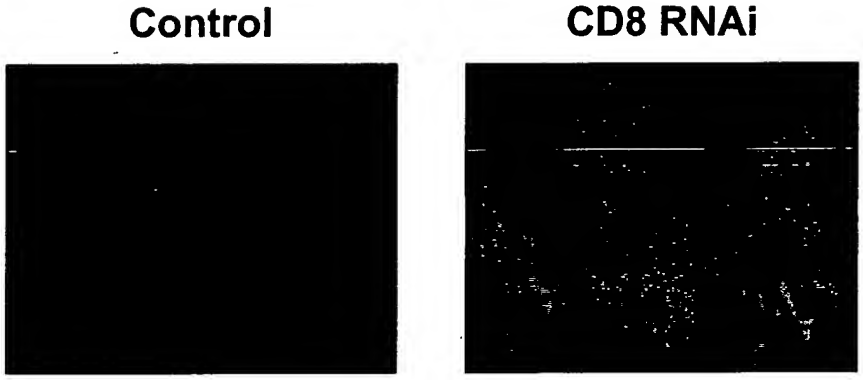

B
Proliferation (counts per minute)
20000
15000
10000
5000
0
Control Virus
CD25 RNAi Virus
0
1
10
100
ng/μl IL-2

Figure 21

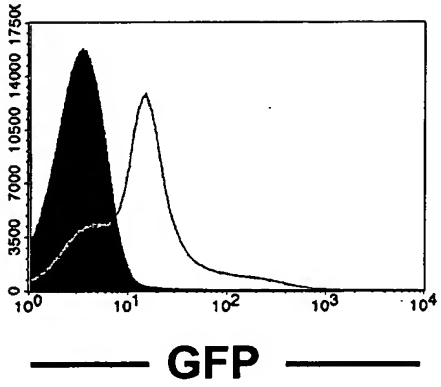
A



B



C



D

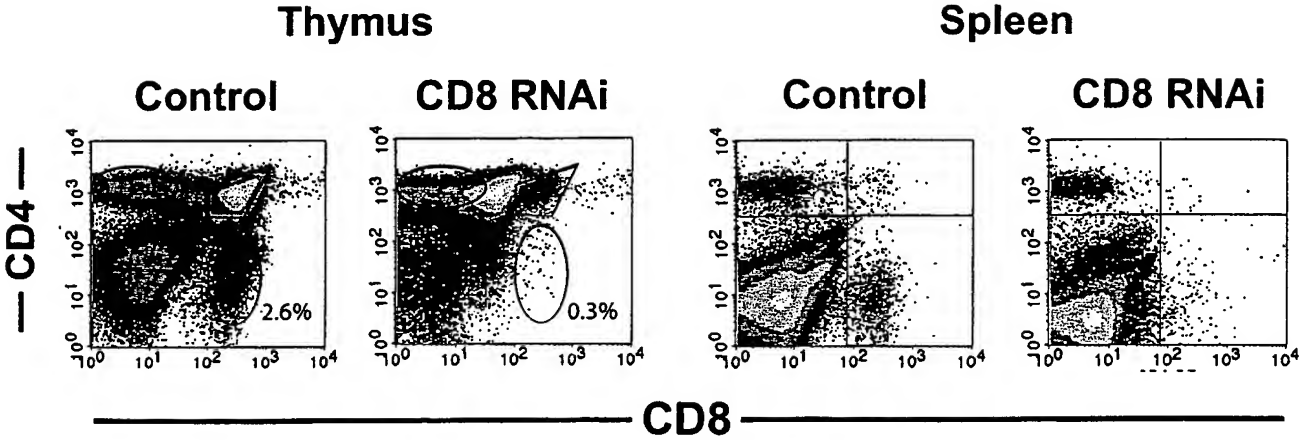
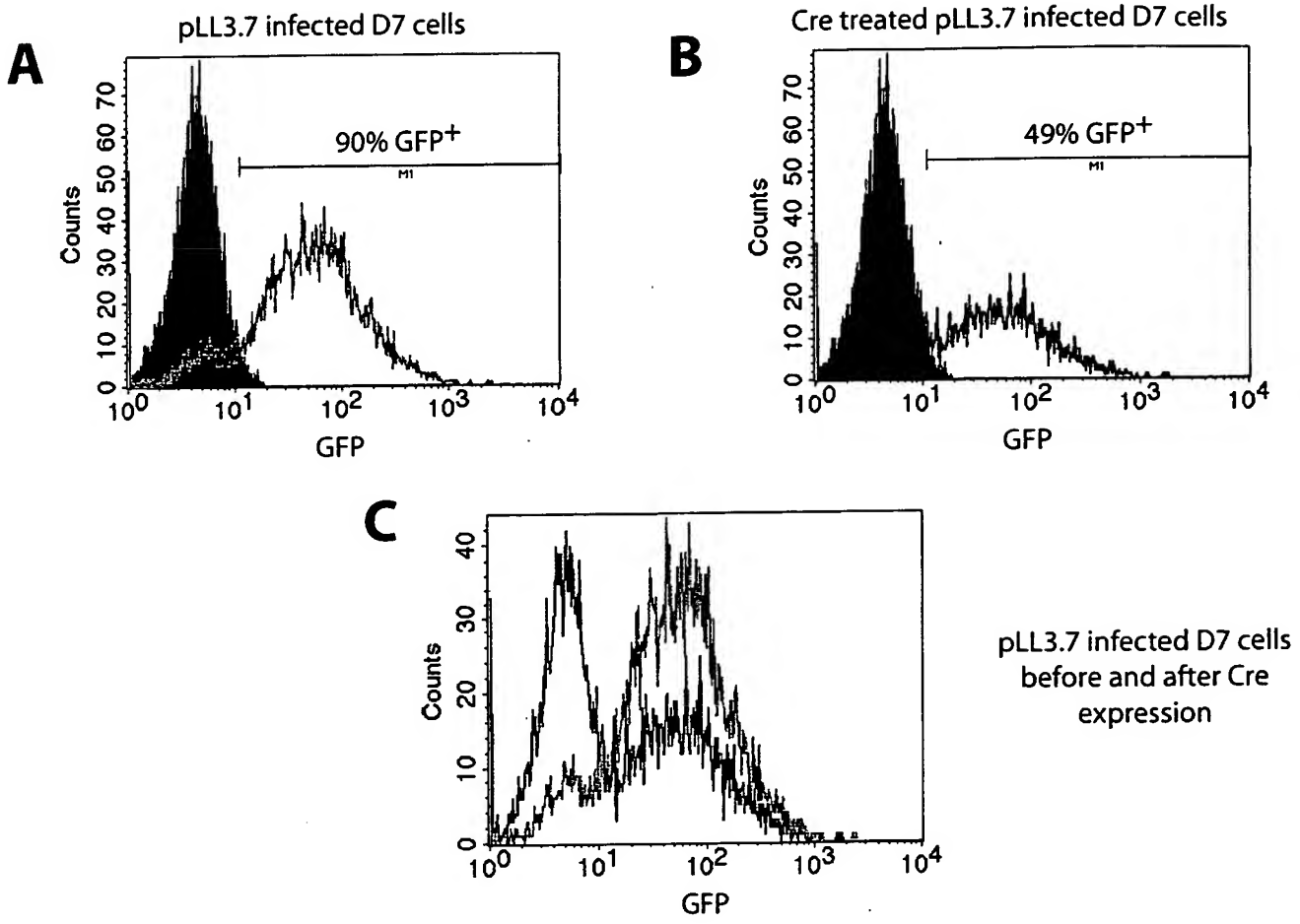


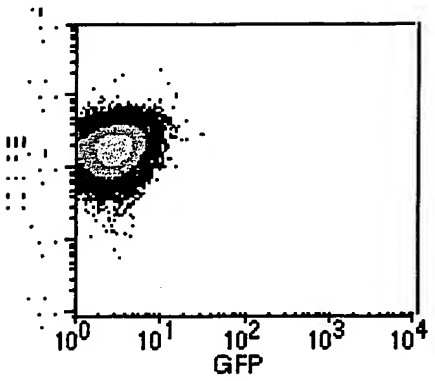
FIGURE 22



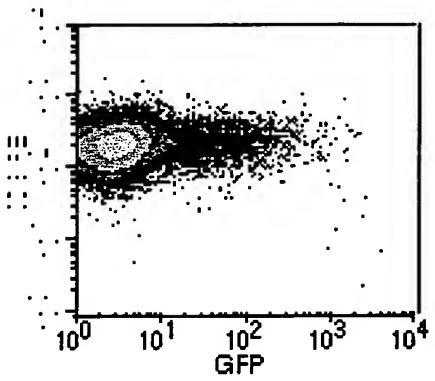
pLL3.7 infected D7 cells before and after Cre expression

A 50% confluent 10cm plate of D7 cells (Bear et al. 2000), was infected with 100ul of concentrated pLL3.7 B-catenin lentivirus, which expressed GFP as a transgene between two LoxP sites. Infected cells were sorted based upon expression of EGFP (**A, green line**). A 50% confluent 6cm-plate of sorted D7 pLL3.7 b-catenin cells was infected with adenovirus expressing the Cre recombinase. 1x10^5 infectious units were used in the infection. Cells were expanded for 10 days to allow for expression of Cre protein, deletion of lox-CMVgfp-lox, and depletion of EGFP protein pools. Cells were then analyzed by flow cytometry for expression of EGFP (**B, pink line**). Cells were also sorted based upon loss of EGFP expression and expanded. Purple solid peak in A and B represent uninfected control. Percentage GFP$^+$ cells are shown on each plot. A direct comparison between pLL3.7 infected D7 cells before (**green line**) and after (**pink line**) Cre delivery is seen in **C**.

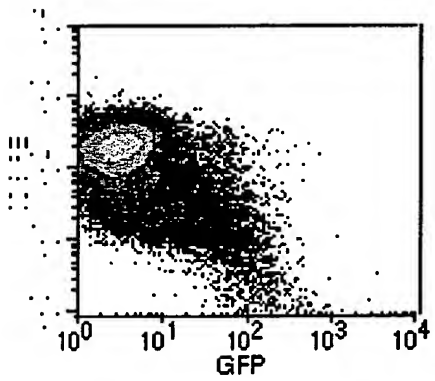
Figure 23



untransfected



transfected w/
irrelevant stem loop



cd8 stem loop in LL2.7

Figure 24

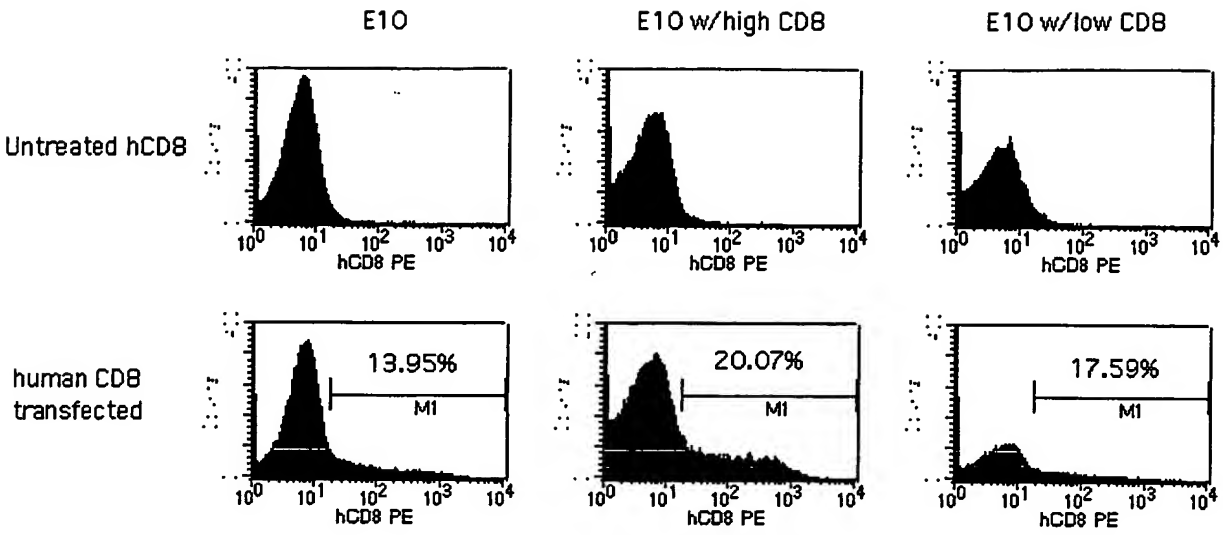

E10
E10 w/high CD8
E10 w/low CD8
Untreated hCD8
human CD8 transfected
13.95%
20.07%
17.59%
M1
hCD8 PE

Figure 25